69 -continued

aatottoato agttogtaag ttottttata gaagtoatta gottotaagg tgattatatt	120
ttagtattaa attttgctaa ttgcttgcta taaagttgaa atgtctaatg cttaaatgaa	180
cacttttttg aagctgacat acgaatacat catatcatat	240
gtccttgaag tctggcattg acagtcacca ggctgttctc agtagtctgt ccttggaagc	300
tcttggggag acaaaaagag gtcccagaga gtcccaacag gttggcataa ggtcattaac	360
accagcatag teggetegae caagaetgta agegagtega titeaactaa aaagattatt	420
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gccacaggcc gatacaa	497
<210> SEQ ID NO 76 <211> LENGTH: 234 <212> TYPE: DNA <213> ORGANISM: Lake Victoria marburgvirus	
<400> SEQUENCE: 76	
gaagaacatt aagaaaaagg atgttettat tttteaaeta aaettgeata teetttgttg	60
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ccccaaattt tcaatcatac acataataac cattttagta gcgttacctt tcaatacaat	180
ctaggtgatt gtgaaaagac ttccaaacat ggcagaatta tcaacgcgtt acaa	234

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It is claimed:

1. A method of treating Marburg virus infection in a subject, the method comprising:

administering to a subject a therapeutically effective 35 amount of an antisense oligomer of 12-40 morpholino subunits linked by phosphorous-containing intersubunit linkages which join a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, 40 wherein at least 2 and no more than half of the total number of intersubunit linkages are positively charged at physiological pH; and comprising

a targeting sequence which forms a heteroduplex with a ⁴⁵ target sequence of the AUG start-site region of a positive-strand mRNA for Marburg viral protein NP;

wherein the antisense oligomer inhibits virus production.

- **2**. The method of claim **1**, wherein the targeting sequence forms a heteroduplex with the AUG start-site region defined by SEQ ID NO:13.
- 3. The method of claim 2, wherein the targeting sequence is 55 complementary to at least 12 contiguous bases of the sequence of SEQ ID NO:13.
- **4**. The method of claim **2**, wherein the antisense oligomer has 15-25 subunits.
- **5**. The method of claim **2**, wherein the heteroduplex has a Tm of dissociation of at least 45° C.
- **6.** The method of claim **1**, wherein the morpholino subunits are joined by intersubunit linkages in accordance with the structure:

$$Z = P - X$$
 $Y_1 = 0$
 $Y_2 = 0$
 $Y_3 = 0$
 $Y_4 = 0$
 $Y_$

wherein Y_1 is 0, Z is 0, P_j is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide, and X is alkyl alkoxy; thioalkoxy; —NR₂, wherein each R is independently H or lower alkyl; or 1-piperazino.

- 7. The method of claim 3, wherein the targeting sequence is complementary to at least 14-15 bases that are upstream of the AUG start codon.
- 8. The method of claim 7, wherein the targeting sequence is complementary to at least 20 bases that are upstream of the AUG start codon, and wherein the antisense oligomer has between 2-8 piperazine-containing intersubunit linkages, and at least one inosine base-pairing moiety.
- 9. The method of claim 1, which further includes administering to the subject a therapeutically effective amount of a second antisense oligomer wherein the targeting sequence of the second antisense oligomer forms a heteroduplex with the AUG start-site region defined by SEQ ID NO: 9.
- 10. The method of claim 9, wherein the targeting sequence of the second antisense oligomer is complementary to at least 12 contiguous bases of the sequence of SEQ ID NO:9.